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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=24; hr=12; min=35; sec=11; ms=947;]

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Application No: 10536802 Version No: 3.0

Input Set:

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Finished: 2009-03-06 23:42:38.089
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 771 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

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SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY AGENCY

Tsukasa SEYA

Misako MATSUMOTO

Hiroyuki OSHIUMI

<120> Novel Adaptor Protein that Binds to Mammalian Toll-Like Receptor 3,
and Gene Thereof

<130> 1035-591 / A211-02/US

<140> 10536802

<141> 2009-03-06

<150> PCT/JP2003/014854

<151> 2003-11-20

<150> JP 2002-349015

<151> 2002-11-29

<160> 12

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Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu

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ggt gca gca ggc cag gac aag ctc ttg tat ctg aag cac aaa ctg aag 155

Gly Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys

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acc cca cgc cca ggc tgc cag ggg cag gac ctc ctg cat gcc atg gtt 203

Thr Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val

35 40 45

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Leu Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala

50 55 60

ttg aag gcc gat gcg gtg gcc cgg ctg gtg gcc cgc cag tgg gct ggc 299

Leu Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly

65 70 75

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Val Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala			
80	85	90	95
gtg gcc cgc ttg tac cac ctg ctg gct gag gag aag ctg tgc ccc gcc			395
Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala			
100	105	110	
tcg ctg cgg gac gtg gcc tac cag gaa gcc gtc cgc acc ctc agc tcc			443
Ser Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser			
115	120	125	
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Arg Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg			
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Cys Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln			
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Ser Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr			
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agg agc ctc cca cgc ccc att gac ggt gtt tcg gac tgg agc caa ggg			635
Arg Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly			
180	185	190	
tgc tcc ctg cga tcc act ggc agc cct gcc tcc ctg gcc agc aac ttg			683
Cys Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu			
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Glu Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser			
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Pro His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val			
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Pro Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp			
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Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu			
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tcc tcc ctg gaa tca tca tcg gaa cag aaa ttc tat aac ttt gtg atc Ser Ser Leu Glu Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile	385	390	395	1259	
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ctg gag gcc ctt ggc gtg ccc gac ggg gcc acc ttc tgc gag gat ttc Leu Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe	420	425	430	1355	
cag gtg ccg ggg cgc ggg gag ctg agc tgc ctg cag gac gcc ata gac Gln Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp	435	440	445	1403	
cac tca gct ttc atc atc cta ctt ctc acc tcc aac ttc gac tgt cgc His Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg	450	455	460	1451	
ctg agc ctg cac cag gtg aac caa gcc atg atg agc aac ctc acg cga Leu Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg	465	470	475	1499	
cag ggg tcg cca gac tgt gtc atc ccc ttc ctg ccc ctg gag agc tcc Gln Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser	480	485	490	495	1547
ccg gcc cag ctc agc tcc gac acg gcc agc ctg ctc tcc ggg ctg gtg Pro Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val	500	505	510	1595	
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 Arg Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln
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 Ser Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe
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 Trp Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly
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 Thr Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu
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 Pro Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro
 660 665 670
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 Gln Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val
 675 680 685
 cag ctg ggg ctg aac aac cac atg tgg aac cag aga ggg tcc cag gcg 2171
 Gln Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala
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 Pro Glu Asp Lys Thr Gln Glu Ala Glu
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Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
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85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
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Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
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Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
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Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
195 200 205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
210 215 220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225 230 235 240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
245 250 255

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Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
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Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
290 295 300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
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325 330 335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
340 345 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser
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Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
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His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
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Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
435 440 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
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Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
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Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
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Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
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Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
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Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
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Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val
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Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp
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